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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file seq1-25-41.res made by tport on Mon 14 Aug 106 16:55:49-PDT.

Query sequence being compared: SEQ1-25-41 (1-17)
Number of sequences searched: 23
Number of scores above cutoff: 12

Results of the initial comparison of SEQ1-25-41 (1-17) with:
File : US10825908A.seq

```

100-
N -
U 50-
M -
B -
E -
R -
O *
F 10-
S -
E 5-
Q -
U -
N -
C -
E -
S 0
SCORE 0 | 2 | 4 | 6 | 8 | 9 | 11 | 13 | 15 | 17 |
STDEV 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |

```

PARAMETERS

Similarity matrix Unitary K-tuple
Mismatch penalty 1 Joining penalty 4
Gap penalty 5.00 Window size 30
Gap size penalty 0.33
Cutoff score 1
Randomization group 0

SEARCH STATISTICS

Scores: Mean Median Standard Deviation
5 1 6.70
Times: CPU
00:00:00.00 Total Elapsed
00:00:00.00
Number of residues: 788
Number of sequences searched: 23
Number of scores above cutoff: 12

The scores below are sorted by initial score.
Significance is calculated based on initial score.

100% similar sequences to the query sequence were found:

Sequence Name	Description	Int. Opt.	Length	Score	Sig.	Frame
1						

```

-----
1. US-10-825-908A-1 Sequence 19, Application 60 17 17 1.79 0
2. US-10-825-908A-9 Sequence 9, Application U 58 17 17 1.79 0

```

1. SEQ1-25-41 (1-17)
US-10-825-908A-1 Sequence 19, Application US/10825908A

Initial Score = 17 Optimized Score = 17 Significance = 1.79
Residue Identity = 100% Matches = 17 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

```

X
AATCAAAAGCGAATGCG
|||||
AATCAAAAGCGAATGCGTATGTCGTAGGCACTAGCAAAAGCAAGTGAAGAAAG
X 10 X 20 30 40 50 60

```

2. SEQ1-25-41 (1-17)
US-10-825-908A-9 Sequence 9, Application US/10825908A

Initial Score = 17 Optimized Score = 17 Significance = 1.79
Residue Identity = 100% Matches = 17 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

```

X
AATCAAAAGCGAATGCG
|||||
AATCAAAAGCGAATGCGTATGTCGTAGGCACTAGCAAAAGCAAGTGAAGAAAG
X 10 X 20 30 40 50

```

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Release 5.4

Results file seq2-25-41-inv.res made by tport on Mon 14 Aug 106 16:59:05-PDT.

Query sequence being compared: SEQ2-25-41' (1-17)
Number of sequences searched: 23
Number of scores above cutoff: 9

Results of the initial comparison of SEQ2-25-41' (1-17) with:
File : US10825908A.seq

```

100- -
N - -
U 50- -
M - -
B - -
E - -
R - -
O * -
F 10- -
S - -
E 5- -
U - -
N - -
C - -
E - -
S 0-----2-----4-----5-----7-----9-----11-----12-----14-----16-----
SCORE 0| | | | | | | | | | | | | | | |
STDDEV 0| | | | | | | | | | | | | | | |

```

PARAMETERS

Similarity matrix Unitary 4
Mismatch penalty 1 K-tuple 30
Gap penalty 5.00 Joining penalty 17
Gap size penalty 0.33 Window size
Cutoff score 0
Randomization group 0

SEARCH STATISTICS

Scores: Mean 3 Median 1 Standard Deviation 4.80
Times: CPU 1
00:00:00.00 Total Elapsed
Number of residues: 788
Number of sequences searched: 23
Number of scores above cutoff: 9

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name Description Length Score Score Sig. Frame

**** 2 standard deviations above mean ****

1. US-10-825-908A-9 Sequence 9, Application U 58 16 16 2.71 0
2. US-10-825-908A-1 Sequence 19, Application 60 16 16 2.71 0

1. SEQ2-25-41' (1-17)

US-10-825-908A-9 Sequence 9, Application US/10825908A

Initial Score = 16 Optimized Score = 16 Significance = 2.71
Residue Identity = 100% Matches = 16 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

```

AATCAAAAGCGAATGCGTATGCTGTGAGGCACTAGCMAAGCTGCAAAAGATGAAGAG
10 20 30 40 50
X 10 X
GCAAAAGATGAAGAGT
|||||

```

2. SEQ2-25-41' (1-17)
US-10-825-908A-1 Sequence 19, Application US/10825908A

Initial Score = 16 Optimized Score = 16 Significance = 2.71
Residue Identity = 100% Matches = 16 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

```

AATCAAAAGCGAATGCGTATGCTGTGAGGCACTAGCMAAGCTGCAAAAGATGAAGAG
10 20 30 40 50
X 10 X
GCAAAAGATGAAGAGT
|||||

```